

SEQUENCE LISTING

<110> Langermann, Solomon R.
Hultgren, Scott J.
Hung, Chia-Suei
Bouckaert, Julie

<120> Mutant Proteins, High Potency Inhibitory Antibodies, and FimCH
Crystal Structure

<130> 10271-037

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<170> PatentIn version 3.0

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<212> DNA

<213> E. coli

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tgc ttg ctg gca ggt atc ctg atg ttc atg gca atg atg gtt gcc gga 96

Cys Leu Leu Ala Gly Ile Leu Met Phe Met Ala Met Met Val Ala Gly
20 25 30

cgc gct gaa gcg gga gtg gcc tta ggt gcg act cgc gta att tat ccg 144

Arg Ala Glu Ala Gly Val Ala Leu Gly Ala Thr Arg Val Ile Tyr Pro
35 40 45

gca ggg caa aaa caa gtg caa ctt gcc gtg aca aat aat gat gaa aat 192

Ala Gly Gln Lys Gln Val Gln Leu Ala Val Thr Asn Asn Asp Glu Asn
50 55 60

agt acc tat tta att caa tca tgg gtg gaa aat gcc gat ggt gta aag 240

Ser Thr Tyr Leu Ile Gln Ser Trp Val Glu Asn Ala Asp Gly Val Lys
65 70 75 80

gat ggt cgt ttt atc gtg acg cct cct ctg ttt gcg atg aag gga aaa 288

Asp Gly Arg Phe Ile Val Thr Pro Pro Leu Phe Ala Met Lys Gly Lys
85 90 95

aaa gag aat acc tta cgt att ctt gat gca aca aat aac caa ttg cca 336

Lys Glu Asn Thr Leu Arg Ile Leu Asp Ala Thr Asn Asn Gln Leu Pro
100 105 110

cag gac cgg gaa agt tta ttc tgg atg aac gtt aaa gcg att ccg tca 384

Gln Asp Arg Glu Ser Leu Phe Trp Met Asn Val Lys Ala Ile Pro Ser
115 120 125

atg gat aaa tca aaa ttg act gag aat acg cta cag ctc gca att atc	432
Met Asp Lys Ser Lys Leu Thr Glu Asn Thr Leu Gln Leu Ala Ile Ile	
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agc cgc att aaa ctg tac tat cgc ccg gct aaa tta gcg ttg cca ccc	480
Ser Arg Ile Lys Leu Tyr Tyr Arg Pro Ala Lys Leu Ala Leu Pro Pro	
145 150 155 160	
gat cag gcc gca gaa aaa tta aga ttt cgt cgt agc gcg aat tct ctg	528
Asp Gln Ala Ala Glu Lys Leu Arg Phe Arg Arg Ser Ala Asn Ser Leu	
165 170 175	
acg ctg att aac ccg aca ccc tat tac ctg acg gta aca gag ttg aat	576
Thr Leu Ile Asn Pro Thr Pro Tyr Tyr Leu Thr Val Thr Glu Leu Asn	
180 185 190	
gcc gga acc cgg gtt ctt gaa aat gca ttg gtg cct cca atg ggc gaa	624
Ala Gly Thr Arg Val Leu Glu Asn Ala Leu Val Pro Pro Met Gly Glu	
195 200 205	
agc acg gtt aaa ttg cct tct gat gca gga agc aat att act tac cga	672
Ser Thr Val Lys Leu Pro Ser Asp Ala Gly Ser Asn Ile Thr Tyr Arg	
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Arg Ala Glu Ala Gly Val Ala Leu Gly Ala Thr Arg Val Ile Tyr Pro	
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Ser Thr Tyr Leu Ile Gln Ser Trp Val Glu Asn Ala Asp Gly Val Lys	
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Asp Gly Arg Phe Ile Val Thr Pro Pro Leu Phe Ala Met Lys Gly Lys	
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Lys Glu Asn Thr Leu Arg Ile Leu Asp Ala Thr Asn Asn Gln Leu Pro	
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Gln Asp Arg Glu Ser Leu Phe Trp Met Asn Val Lys Ala Ile Pro Ser	
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Ser Arg Ile Lys Leu Tyr Tyr Arg Pro Ala Lys Leu Ala Leu Pro Pro	
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Asp Gln Ala Ala Glu Lys Leu Arg Phe Arg Arg Ser Ala Asn Ser Leu	
165 170 175	

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Val Pro Thr Gly Gly Cys Asp Val Ser Ala Arg Asp Val Thr Val Thr	
160 165 170	
ctg ccg gac tac cct ggt tca gtg cca att cct ctt acc gtt tat tgt	624
Leu Pro Asp Tyr Pro Gly Ser Val Pro Ile Pro Leu Thr Val Tyr Cys	
175 180 185	
gcg aaa agc caa aac ctg ggg tat tac ctc tcc ggc aca acc gca gat	672
Ala Lys Ser Gln Asn Leu Gly Tyr Tyr Leu Ser Gly Thr Thr Ala Asp	
190 195 200	
gcg ggc aac tcg att ttc acc aat acc gcg tcg ttt tca cct gca cag	720
Ala Gly Asn Ser Ile Phe Thr Asn Thr Ala Ser Phe Ser Pro Ala Gln	
205 210 215	
ggc gtc ggc gta cag ttg acg cgc aac ggt acg att att cca gcg aat	768
Gly Val Gly Val Gln Leu Thr Arg Asn Gly Thr Ile Ile Pro Ala Asn	
220 225 230 235	
aac acg gta tcg tta gga gca gta ggg act tcg gcg gtg agt ctg gga	816
Asn Thr Val Ser Leu Gly Ala Val Gly Thr Ser Ala Val Ser Leu Gly	
240 245 250	
tta acg gca aat tat gca cgt acc gga ggg cag gtg act gca ggg aat	864
Leu Thr Ala Asn Tyr Ala Arg Thr Gly Gly Gln Val Thr Ala Gly Asn	
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Pro Ile Gly Gly Gly Ser Ala Asn Val Tyr Val Asn Leu Ala Pro Val	
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Cys His Asn Asp Tyr Pro Glu Thr Ile Thr Asp Tyr Val Thr Leu Gln	
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Arg Gly Ser Ala Tyr Gly Gly Val Leu Ser Asn Phe Ser Gly Thr Val	
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Lys Tyr Ser Gly Ser Ser Tyr Pro Phe Pro Thr Thr Ser Glu Thr Pro	
80 85 90	
Arg Val Val Tyr Asn Ser Arg Thr Asp Lys Pro Trp Pro Val Ala Leu	
95 100 105	
Tyr Leu Thr Pro Val Ser Ser Ala Gly Gly Val Ala Ile Lys Ala Gly	
110 115 120	

Ser Leu Ile Ala Val Leu Ile Leu Arg Gln Thr Asn Asn Tyr Asn Ser
125 130 135
Asp Asp Phe Gln Phe Val Trp Asn Ile Tyr Ala Asn Asn Asp Val Val
140 145 150 155
Val Pro Thr Gly Gly Cys Asp Val Ser Ala Arg Asp Val Thr Val Thr
160 165 170
Leu Pro Asp Tyr Pro Gly Ser Val Pro Ile Pro Leu Thr Val Tyr Cys
175 180 185
Ala Lys Ser Gln Asn Leu Gly Tyr Tyr Leu Ser Gly Thr Thr Ala Asp
190 195 200
Ala Gly Asn Ser Ile Phe Thr Asn Thr Ala Ser Phe Ser Pro Ala Gln
205 210 215
Gly Val Gly Val Gln Leu Thr Arg Asn Gly Thr Ile Ile Pro Ala Asn
220 225 230 235
Asn Thr Val Ser Leu Gly Ala Val Gly Thr Ser Ala Val Ser Leu Gly
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Leu Thr Ala Asn Tyr Ala Arg Thr Gly Gly Gln Val Thr Ala Gly Asn
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<210> 44
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